

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/591,447ADATE: 12/10/97
TIME: 15:13:45

INPUT SET: S22013.raw

This Raw Listing contains the General
Information Section and up to the first 50 pages.

SEQUENCE LISTING

1
2
3 (1) General Information:
4
5 (i) APPLICANT: QUENTIN-MILLET al., Marie-Jose et
6
7 (ii) TITLE OF INVENTION: TBP2 FRAGMENTS OF THE TRANSFERRIN
8 RECEPTOR OF NEISSERIA MENINGITIDIS
9
10 (iii) NUMBER OF SEQUENCES: 44
11
12 (iv) CORRESPONDENCE ADDRESS:
13 (A) ADDRESSEE: LARSON AND TAYLOR
14 (B) STREET: 1199 NORTH FAIRFAX STREET
15 (C) CITY: ALEXANDRIA
16 (D) STATE: VIRGINIA
17 (E) COUNTRY: USA
18 (F) ZIP: 22314
19
20 (v) COMPUTER READABLE FORM:
21 (A) MEDIUM TYPE: Floppy disk
22 (B) COMPUTER: IBM PC compatible
23 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
24 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
25
26 (vi) CURRENT APPLICATION DATA:
27 (A) APPLICATION NUMBER: US 08/591,447
28 (B) FILING DATE: 29-JAN-1996
29 (C) CLASSIFICATION:
30
31 (viii) ATTORNEY/AGENT INFORMATION:
32 (A) NAME: SARRO, THOMAS P
33 (B) REGISTRATION NUMBER: 19,196
34 (C) REFERENCE/DOCKET NUMBER: XI/P02956
35
36 (ix) TELECOMMUNICATION INFORMATION:
37 (A) TELEPHONE: 703-739-4900
38 (B) TELEFAX: 703-739-9577
39
40
41 (2) INFORMATION FOR SEQ ID NO:1:
42
43 (i) SEQUENCE CHARACTERISTICS:
44 (A) LENGTH: 2230 base pairs
45 (B) TYPE: nucleic acid
46 (C) STRANDEDNESS: single

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47 (D) TOPOLOGY: linear
48
49 (ii) MOLECULE TYPE: DNA (genomic)
50
51 (vi) ORIGINAL SOURCE:
52 (A) ORGANISM: Neisseria meningitidis
53 (B) STRAIN: IM2169
54
55 (ix) FEATURE:
56 (A) NAME/KEY: sig_peptide
57 (B) LOCATION: 60..119
58
59 (ix) FEATURE:
60 (A) NAME/KEY: mat_peptide
61 (B) LOCATION: 120..2192
62
63 (ix) FEATURE:
64 (A) NAME/KEY: CDS
65 (B) LOCATION: 60..2192
66
67 (ix) FEATURE:
68 (A) NAME/KEY: misc_feature
69 (B) LOCATION: 120..1154
70
71 (ix) FEATURE:
72 (A) NAME/KEY: misc_feature
73 (B) LOCATION: 1155..1748
74
75 (ix) FEATURE:
76 (A) NAME/KEY: misc_feature
77 (B) LOCATION: 1749..2192
78
79 (ix) FEATURE:
80 (A) NAME/KEY: misc_binding
81 (B) LOCATION: 237..1169
82
83
84 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
85
86 ATTTGTTAAA AATAAATAAA ATAATAATCC TTATCATTCT TTAATTGAAT TGGGTTTAT 59
87
88 ATG AAC AAT CCA TTG GTA AAT CAG GCT GCT ATG GTG CTG CCT GTG TTT 107
89 Met Asn Asn Pro Leu Val Asn Gln Ala Ala Met Val Leu Pro Val Phe
90 -20 -15 -10 -5
91
92 TTG TTG AGT GCC TGT CTG GGC GGC GGC GGC AGT TTC GAT CTT GAT TCT 155
93 Leu Leu Ser Ala Cys Leu Gly Gly Gly Gly Ser Phe Asp Leu Asp Ser
94 1 5 10
95
96 GTC GAT ACC GAA GCC CCG CGT CCC GCG CCA AAG TAT CAA GAT GTT TCT 203
97 Val Asp Thr Glu Ala Pro Arg Pro Ala Pro Lys Tyr Gln Asp Val Ser
98 15 20 25
99

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100	TCC GAA AAA CCG CAA GCC CAA AAA GAC CAA GGC GGA TAC GGT TTT GCG	251
101	Ser Glu Lys Pro Gln Ala Gln Lys Asp Gln Gly Gly Tyr Gly Phe Ala	
102	30 35 40	
103		
104	ATG AGG TTG AAA CGG AGG AAT TGG TAT CCG GGG GCA GAA GAA AGC GAG	299
105	Met Arg Leu Lys Arg Arg Asn Trp Tyr Pro Gly Ala Glu Glu Ser Glu	
106	45 50 55 60	
107		
108	GTT AAA CTG AAC GAG AGT GAT TGG GAG GCG ACG GGA TTG CCG ACA AAA	347
109	Val Lys Leu Asn Glu Ser Asp Trp Glu Ala Thr Gly Leu Pro Thr Lys	
110	65 70 75	
111		
112	CCC AAG GAA CTT CCT AAA CGG CAA AAA TCG GTT ATT GAA AAA GTA GAA	395
113	Pro Lys Glu Leu Pro Lys Arg Gln Lys Ser Val Ile Glu Lys Val Glu	
114	80 85 90	
115		
116	ACA GAC GGC GAC AGC GAT ATT TAT TCT TCC CCC TAT CTC ACA CCA TCA	443
117	Thr Asp Gly Asp Ser Asp Ile Tyr Ser Ser Pro Tyr Leu Thr Pro Ser	
118	95 100 105	
119		
120	AAC CAT CAA AAC GGC AGC GCT GGC AAC GGT GTA AAT CAA CCT AAA AAT	491
121	Asn His Gln Asn Gly Ser Ala Gly Asn Gly Val Asn Gln Pro Lys Asn	
122	110 115 120	
123		
124	CAG GCA ACA GGT CAC GAA AAT TTC CAA TAT GTT TAT TCC GGT TGG TTT	539
125	Gln Ala Thr Gly His Glu Asn Phe Gln Tyr Val Tyr Ser Gly Trp Phe	
126	125 130 135 140	
127		
128	TAT AAA CAT GCA GCG AGT GAA AAA GAT TTC AGT AAC AAA AAA ATT AAG	587
129	Tyr Lys His Ala Ala Ser Glu Lys Asp Phe Ser Asn Lys Lys Ile Lys	
130	145 150 155	
131		
132	TCA GGC GAC GAT GGT TAT ATC TTC TAT CAC GGT GAA AAA CCT TCC CGA	635
133	Ser Gly Asp Asp Gly Tyr Ile Phe Tyr His Gly Glu Lys Pro Ser Arg	
134	160 165 170	
135		
136	CAA CTT CCT GCT TCT GGA AAA GTT ATC TAC AAA GGT GTG TGG CAT TTT	683
137	Gln Leu Pro Ala Ser Gly Lys Val Ile Tyr Lys Gly Val Trp His Phe	
138	175 180 185	
139		
140	GTA ACC GAT ACA AAA AAG GGT CAA GAT TTT CGT GAA ATT ATC CAG CCT	731
141	Val Thr Asp Thr Lys Lys Gly Gln Asp Phe Arg Glu Ile Ile Gln Pro	
142	190 195 200	
143		
144	TCA AAA AAA CAA GGC GAC AGG TAT AGC GGA TTT TCT GGT GAT GGC AGC	779
145	Ser Lys Lys Gln Gly Asp Arg Tyr Ser Gly Phe Ser Gly Asp Gly Ser	
146	205 210 215 220	
147		
148	GAA GAA TAT TCC AAC AAA AAC GAA TCC ACG CTG AAA GAT GAT CAC GAG	827
149	Glu Glu Tyr Ser Asn Lys Asn Glu Ser Thr Leu Lys Asp Asp His Glu	
150	225 230 235	
151		
152	GGT TAT GGT TTT ACC TCG AAT TTA GAA GTG GAT TTC GGC AAT AAG AAA	875

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153	Gly Tyr Gly Phe Thr Ser Asn Leu Glu Val Asp Phe Gly Asn Lys Lys	
154	240 245 250	
155		
156	TTG ACG GGT AAA TTA ATA CGC AAT AAT GCG AGC CTA AAT AAT AAT ACT	923
157	Leu Thr Gly Lys Leu Ile Arg Asn Asn Ala Ser Leu Asn Asn Asn Thr	
158	255 260 265	
159		
160	AAT AAT GAC AAA CAT ACC ACC CAA TAC TAC AGC CTT GAT GCA CAA ATA	971
161	Asn Asn Asp Lys His Thr Thr Gln Tyr Tyr Ser Leu Asp Ala Gln Ile	
162	270 275 280	
163		
164	ACA GGC AAC CGC TTC AAC GGC ACG GCA ACG GCA ACT GAC AAA AAA GAG	1019
165	Thr Gly Asn Arg Phe Asn Gly Thr Ala Thr Ala Thr Asp Lys Lys Glu	
166	285 290 295 300	
167		
168	AAT GAA ACC AAA CTA CAT CCC TTT GTT TCC GAC TCG TCT TCT TTG AGC	1067
169	Asn Glu Thr Lys Leu His Pro Phe Val Ser Asp Ser Ser Ser Leu Ser	
170	305 310 315	
171		
172	GGC GGC TTT TTC GGC CCG CAG GGT GAG GAA TTG GGT TTC CGC TTT TTG	1115
173	Gly Gly Phe Phe Gly Pro Gln Gly Glu Glu Leu Gly Phe Arg Phe Leu	
174	320 325 330	
175		
176	AGC GAC GAT CAA AAA GTT GCC GTT GTC GGC AGC GCG AAA ACC AAA GAC	1163
177	Ser Asp Asp Gln Lys Val Ala Val Gly Ser Ala Lys Thr Lys Asp	
178	335 340 345	
179		
180	AAA CTG GAA AAT GGC GCG GCG GCT TCA GGC AGC ACA GGT GCG GCA GCA	1211
181	Lys Leu Glu Asn Gly Ala Ala Ala Ser Gly Ser Thr Gly Ala Ala Ala	
182	350 355 360	
183		
184	TCG GGC GGT GCG GCA GGC ACG TCG TCT GAA AAC AGT AAG CTG ACC ACG	1259
185	Ser Gly Gly Ala Ala Gly Thr Ser Ser Glu Asn Ser Lys Leu Thr Thr	
186	365 370 375 380	
187		
188	GTT TTG GAT GCG GTT GAA TTG ACA CTA AAC GAC AAG AAA ATC AAA AAT	1307
189	Val Leu Asp Ala Val Glu Leu Thr Leu Asn Asp Lys Lys Ile Lys Asn	
190	385 390 395	
191		
192	CTC GAC AAC TTC AGC AAT GCC GCC CAA CTG GTT GTC GAC GGC ATT ATG	1355
193	Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp Gly Ile Met	
194	400 405 410	
195		
196	ATT CCG CTC CTG CCC AAG GAT TCC GAA AGC GGG AAC ACT CAG GCA GAT	1403
197	Ile Pro Leu Leu Pro Lys Asp Ser Glu Ser Gly Asn Thr Gln Ala Asp	
198	415 420 425	
199		
200	AAA GGT AAA AAC GGC GGA ACA GAA TTT ACC CGC AAA TTT GAA CAC ACG	1451
201	Lys Gly Lys Asn Gly Gly Thr Glu Phe Thr Arg Lys Phe Glu His Thr	
202	430 435 440	
203		
204	CCG GAA AGT GAT AAA AAA GAC GCC CAA GCA GGT ACG CAG ACG AAT GGG	1499
205	Pro Glu Ser Asp Lys Lys Asp Ala Gln Ala Gly Thr Gln Thr Asn Gly	

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	445		450		455		460	
206								
207								
208	GCG CAA ACC GCT TCA AAT ACG GCA GGT GAT ACC AAT GGC AAA ACA AAA							1547
209	Ala Gln Thr Ala Ser Asn Thr Ala Gly Asp Thr Asn Gly Lys Thr Lys							
210		465			470		475	
211								
212	ACC TAT GAA GTC GAA GTC TGC TGT TCC AAC CTC AAT TAT CTG AAA TAC							1595
213	Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu Asn Tyr Leu Lys Tyr							
214		480			485		490	
215								
216	GGA ATG TTG ACG CGC AAA AAC AGC AAG TCC GCG ATG CAG GCA GGA GGA							1643
217	Gly Met Leu Thr Arg Lys Asn Ser Lys Ser Ala Met Gln Ala Gly Gly							
218		495			500		505	
219								
220	AAC AGT AGT CAA GCT GAT GCT AAA ACG GAA CAA GTT GAA CAA AGT ATG							1691
221	Asn Ser Ser Gln Ala Asp Ala Lys Thr Glu Gln Val Glu Gln Ser Met							
222		510			515		520	
223								
224	TTC CTC CAA GGC GAG CGT ACC GAT GAA AAA GAG ATT CCA ACC GAC CAA							1739
225	Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro Thr Asp Gln							
226		525			530		535	540
227								
228	AAC GTC GTT TAT CGG GGG TCT TGG TAC GGG CAT ATT GCC AAC GGC ACA							1787
229	Asn Val Val Tyr Arg Gly Ser Trp Tyr Gly His Ile Ala Asn Gly Thr							
230		545			550		555	
231								
232	AGC TGG AGC GGC AAT GCT TCT GAT AAA GAG GGC GGC AAC AGG GCG GAA							1835
233	Ser Trp Ser Gly Asn Ala Ser Asp Lys Glu Gly Gly Asn Arg Ala Glu							
234		560			565		570	
235								
236	TTT ACT GTG AAT TTT GCC GAT AAA AAA ATT ACC GGC AAG TTA ACC GCT							1883
237	Phe Thr Val Asn Phe Ala Asp Lys Lys Ile Thr Gly Lys Leu Thr Ala							
238		575			580		585	
239								
240	GAA AAC AGG CAG GCG CAA ACC TTT ACC ATT GAG GGA ATG ATT CAG GGC							1931
241	Glu Asn Arg Gln Ala Gln Thr Phe Thr Ile Glu Gly Met Ile Gln Gly							
242		590			595		600	
243								
244	AAC GGC TTT GAA GGT ACG GCG AAA ACT GCT GAG TCA GGT TTT GAT CTC							1979
245	Asn Gly Phe Glu Gly Thr Ala Lys Thr Ala Glu Ser Gly Phe Asp Leu							
246		605			610		615	620
247								
248	GAT CAA AAA AAT ACC ACC CGC ACG CCT AAG GCA TAT ATC ACA GAT GCC							2027
249	Asp Gln Lys Asn Thr Thr Arg Thr Pro Lys Ala Tyr Ile Thr Asp Ala							
250		625			630		635	
251								
252	AAG GTA AAG GGC GGT TTT TAC GGG CCT AAA GCC GAA GAG TTG GGC GGA							2075
253	Lys Val Lys Gly Gly Phe Tyr Gly Pro Lys Ala Glu Glu Leu Gly Gly							
254		640			645		650	
255								
256	TGG TTT GCC TAT CCG GGC GAT AAA CAA ACG GAA AAG GCA ACA GCT ACA							2123
257	Trp Phe Ala Tyr Pro Gly Asp Lys Gln Thr Glu Lys Ala Thr Ala Thr							
258		655			660		665	

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SEQUENCE VERIFICATION REPORT
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Original Text